

GENE ENCODING SHORT INTEGUMENTS AND USES THEREOF

This application claims the benefit of U.S. Provisional Patent Application Serial No. ^{60/138,314}~~60/38,316~~, filed June 9, 1999.

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FIELD OF THE INVENTION

10 The invention relates to short integuments¹ nucleic acids and proteins, and to plants having altered phenotypes when transformed with short integuments¹ nucleic acids.

BACKGROUND OF THE INVENTION

15 According to recent estimates, the global demand for crop plants such as rice, wheat, and maize should increase by 40% by 2020. It is thought that classical plant breeding technology, which led to the green revolution in the late 1960s, will contribute less and less to meet this increasing demand, whereas plant genetic engineering will contribute increasingly more. An important thrust area in
20 plant genetic engineering is the identification and use of genes implicated in asexual production of seeds, or "apomixis." Apomixis is thought to be an agronomically desirable trait that should enable seed companies and farmers to lock-in a favorable combination of genes for maximum grain yield without having to lose the gene combination in the next sexual generation. Genes for apomixis
25 have not yet been identified. It is thought that genes that are generally important for very early embryo/seed development may be important for apomixis. A second important thrust is the production of early flowering varieties of plants such that breeding time can be reduced.

30 The evolution of flowering plants may have entailed a modification of primitive leaf or leaf-like structures that contained naked ovules on their surfaces, to specify floral organs that ultimately evolved to surround the ovules (Herr, "The Origin of the Ovule," Am. J. Bot. 82:547-564 (1995); Stebbins,

Flowering Plants: Evolution Above the Species Level, Cambridge, MA: Harvard University Press, pp. 199-245). This view of angiosperm evolution predicts that the genetic regulatory network that controls ovule development should be interlaced with that which triggers flowering. Ovule, as the precursor of seed, is the link to the next generation. Genetic regulatory pathways that are important for early vegetative development of the embryo inside the ovule, for late reproductive development leading to the production of ovules, and for morphogenesis of the haploid female gametophyte, are crucial areas of investigation which can lead to enhanced agricultural practices.

Several genes important for ovule development have been identified in *Arabidopsis thaliana* (Reiser et al., "The Ovule and the Embryo Sac," The Plant Cell 5:1291-1301 (1993)). *BELLI*, a so-called cadastral gene that encodes a homeodomain protein (Reiser et al., "The *BELLI* Gene Encodes a Homeodomain Protein Involved in Pattern Formation in the Arabidopsis Ovule Primordium," Cell 83, 735-742 (1995)), controls the expression of the floral organ identity gene *AG* within the ovule and thereby controls morphogenesis of ovule integuments (Modrusan et al., "Homeotic Transformation of Ovules into Carpel-Like Structures in *Arabidopsis*," The Plant Cell 6:333-349 (1994); Ray et al., "The *Arabidopsis* Floral Homeotic Gene *BELL* (*BELI*) Controls Ovule Development Through Negative Regulation of *AGAMOUS* (*AG*) Gene," Proc. Natl. Acad. Sci. USA 91:5761-5765 (1994)). *SUPERMAN*, another cadastral gene that restricts the spatial expression pattern of the floral organ identity gene *AP3* (Sakai et al., "Role of *SUPERMAN* in Maintaining *Arabidopsis* Floral Whorl Boundaries," Nature 378:199-203 (1995)), is important in ovule integument development (Gaiser et al., "The Arabidopsis *SUPERMAN* Gene Mediates Asymmetric Growth of the Outer Integument of Ovules," The Plant Cell 7:333-345 (1995)). The organ identity gene *AP2* is also known to control ovule morphogenesis (Modrusan et al., "Homeotic Transformation of Ovules into Carpel-Like Structures in *Arabidopsis*," The Plant Cell 6:333-349 (1994)). By contrast, no known meristem identity or flowering control gene had, until now, been demonstrated to have a role in ovule development.

A gene termed SHORT INTEGUMENTS1 (*SINI*), genetically detected in the model plant *Arabidopsis thaliana* by mutational studies has been

determined to be an important regulatory gene for plant reproductive development. The *SIN1* gene is required for normal ovule development (Lang et al., "sin1, A Mutation Affecting Female Fertility in *Arabidopsis*, Interacts with *mod1*, its Recessive Modifier," Genetics 137:1101-1110 (1994); Reiser et al., "The Ovule and the Embryo Sac," The Plant Cell 5:1291-1301 (1993); Robinson-Beers et al., "Ovule Development in Wild-Type *Arabidopsis* and Two Female Sterile Mutants," Plant Cell 4:1237-1250 (1992)). The original isolate of the *sin1* mutation (*sin1-1* allele) was identified as one causing a female sterile phenotype (Robinson-Beers et al., "Ovule Development in Wild-Type *Arabidopsis* and Two Female Sterile Mutants," Plant Cell 4:1237-1250 (1992)). Ovules of the original isolate have short integuments and a defective megagametophyte (see Reiser et al., "The Ovule and the Embryo Sac," The Plant Cell 5:1291-1301 (1993)) for a review on ovule structure; Baker et al., "Interactions Among Genes Regulating Ovule Development in *Arabidopsis thaliana*," Genetics 145:1109-1124 (1997), for a recent genetic analysis; Schneitz et al., "Dissection of Sexual Organ Ontogenesis: A Genetic Analysis of Ovule Development in *Arabidopsis thaliana*," Development 124:1367-1376 (1997), for a summary of the known mutants affected in ovule development). It has been shown that the originally-described *Sin1*⁻ mutant phenotype is a result of an interaction between *sin1*, and *mod1*, its recessive modifier (Lang et al., "sin1, A Mutation Affecting Female Fertility in *Arabidopsis*, Interacts with *mod1*, Its Recessive Modifier," Genetics 137:1101-1110 (1994)), and that *mod1* is *erecta*, a mutation in a putative serine-threonine receptor protein kinase gene. The *sin1-1* or *sin1-2* mutation acting alone causes a defect in the coordination of growth of the two sheets of cells of the inner and outer integuments. All other originally described effects on the ovule, such as the lack of outer integument cell expansion and arrest of the megagametophyte, are due to secondary genetic interactions with *erecta*. There are several prospective protein phosphorylation sites within the SIN1 protein, and these might be substrates of protein kinases, such as the ERECTA product (Torii et al., "The *Arabidopsis* *ERECTA* Gene Encodes a Putative Protein Kinase with Extracellular Leucine-Rich Repeats," Plant Cell 8:735-746 (1996)).

In plants homozygous for the weaker *sin1-2* mutant allele, approximately 40% of all ovules in any flower mature into seeds. But these seeds

frequently contain embryos arrested at different stages of development, some of which germinate to produce abnormal seedlings. Genetic analysis shows that the maternal expression of the *SIN1* gene is necessary for embryo development (Ray et al., "Maternal Effects of the *Short Integument* Mutation on Embryo Development in *Arabidopsis*," Dev. Biol. 180:365-369 (1996)).

Not only does this gene function in the formation of seeds, *SIN1* is the only identified plant gene whose maternal expression is important for pattern formation in the zygotic embryo (Ray et al., "Maternal Effects of the *Short Integument* Mutation on Embryo Development in *Arabidopsis*," Dev. Biol. 180:365-369 (1996)). Both *sin1-1* and *sin1-2* alleles have the maternal-effect embryonic lethality phenotype (Ray et al., "Maternal Effects of the *Short Integument* Mutation on Embryo Development in *Arabidopsis*," Dev. Biol. 180:365-369 (1996)). The wild type *SIN1* allele when transmitted through the pollen is unable to rescue the deleterious effects on embryogenesis of a homozygous maternal *sin1-2* mutation. Ray et al. have shown that a wild type allele of *SIN1* in the endosperm cannot rescue the maternal-effect of *sin1-2* (Ray et al., "Maternal Effects of the *Short Integument* Mutation on Embryo Development in *Arabidopsis*," Dev. Biol. 180:365-369 (1996)). This is the first demonstration of a maternal effect embryonic pattern formation gene in a plant.

In *Arabidopsis thaliana*, meristem development progresses through at least three distinct phases: from vegetative (V) through inflorescence (I) to the floral (F) mode, a process known as the "V → I → F switch." It has been shown that the *sin1* mutation causes a defect in the V → I → F switch. *SIN1* is needed for the expression of the early flowering phenotype imparted by a TERMINAL FLOWER1 (*tfl1*) mutation, and *tfl1 sin1* double mutants do not produce pollen. Furthermore, *sin1-1* allele enhances the effect of an *APETALA1* (*ap1*) mutation. Thus, *SIN1* represents a genetic connection between ovule development and control of flowering.

In addition, the function of *SIN1* gene is important for controlling the time to flower, another important agronomic factor because the timing of seed production depends on the flowering time. Ray et al. have shown by genetic analysis that *SIN1* gene regulates the activity of a master switch gene, LEAFY (*LFY*) that controls flowering time in *Arabidopsis thaliana*. The LEAFY gene

from *Arabidopsis thaliana* was shown to accelerate the flowering time of aspen (an economically important timber plant) from many years to a few months. Additionally, *sin1* mutants are late flowering (Ray et al., "SHORT INTEGUMENT1 (*sin1*), A Gene Required For Ovule Development in *Arabidopsis*, Also Controls Flowering Time," Development 122, 2631-2638 (1996)) due to the production of an excess of vegetative leaves and lateral inflorescence axes before producing the floral primordia, which suggests a role of *SIN1* in meristem fate determination. The ability to improve crop plant production through genetic engineering requires the identification and manipulation of previously unidentified genes that control developmentally important plant processes, including ovule development and flowering in plants.

The present invention is directed to overcoming the deficiencies in the prior art.

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SUMMARY OF THE INVENTION

The present invention relates to an isolated nucleic acid molecule encoding a short integuments1 protein.

The present invention also relates to an isolated short integuments1 protein.

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The present invention also relates to a method of regulating flowering in plants that involves transducing a plant with a DNA molecule encoding a short integuments1 protein under conditions effective to regulate flowering in the plant.

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The present invention also relates to a method of increasing fertility in plants that involves transducing a plant with a DNA molecule encoding a short integuments1 protein under conditions effective to increase fertility.

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The present invention also relates to a method of increasing fecundity in plants that involves transducing a plant with a DNA molecule encoding a short integuments1 protein under conditions effective to increase fecundity.

The present invention also relates to a method of decreasing fertility in plants that involves transducing a plant with a DNA molecule encoding

a short integuments1 protein mutated to cause disruption of the DNA molecule under conditions effective to decrease fertility.

The present invention also relates to an expression vector containing a DNA molecule encoding a short integuments1 protein, and plant
5 cells, plant seeds and transgenic plants transformed with a DNA molecule encoding a short integuments1 protein.

It is expected that elucidation of post-transcriptional regulation in plants will contribute significantly to the ability to control plant production through biotechnology. However, very little is currently understood about
10 mechanisms of post-transcriptional controls, especially in plant reproduction. This invention overcomes this and other deficiencies in the art, as the *SIN1* gene and its encoded protein, which play a vital role in fertility, seed production and flowering time control in plants, provide the agronomist with important tools for engineering the expression of genes involved in seed/embryo development and
15 flowering time.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a map of the chromosomal region overlapping *SIN1* and the functional domains of the predicted SIN1 protein.

20 Figure 2 is a diagram of the BLAST derived homologies of the SIN1 protein.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to an isolated nucleic acid molecule
25 encoding a short integuments1 (SIN1) protein.

One example of the nucleic acid molecule of the present invention is the *SIN1* cDNA molecule, isolated from *Arabidopsis thaliana*, which has a nucleotide sequence corresponding to SEQ. ID. No. 1 as follows:

30 gaagacgaag agagaaacag aacagagtag ggatcgatag accgtggaat ctcaaatca 60
caaacacttt gcaaaagggt tttcaattcc tatttattta caaagaaatc atcaatagta 120
gtgggtctcta ggggttttgct tgctcttctt cgtgaccctt ttttacctgc aaacaacaac 180
ttcaaaattg gcgtgtttcg tacggtctat ctaaccctaa tctgtcacia aacactcttc 240

ttctctcacc cctttttctg ggtttattca attctcgtgc ttttggttct gttttcttct 300
ctgggggattt ggttttcttg agtgagtttt tctcctcttt cttatgttct tgatttgatt 360
attatataga attatggtaa tggaggatga gcctagagaa gccacaataa agccttctta 420
ttggctagat gcttgcgagg acatctcttg tgatcttctc gatgatctcg tgtctgaatt 480
5 tgatccttcc tctgttgctg tcaatgaatc cactgatgaa aacggcgtca tcaatgattt 540
tttcggtggg attgatcaca ttttagatag tatcaagaac ggtggaggct taccaaaca 600
tggcgtttct gataccaatt ctcaaataa cgaggttact gtaactcctc aggttattgc 660
taaggagaca gtgaaggaga atgggttgca aaagaatggc ggtaagagag acgaattctc 720
gaaagaggaa ggagacaagg ataggaagag agctaggggt tgtagttatc agagtgaag 780
10 gagtaacctt tcaggtagag ggcattgtta taattctagg gagggagata ggtttatgaa 840
taggaaacgt actcgtaatt gggacgaggc gggttaacaat aagaagaaaa gggaatgtaa 900
caattacaga agagatggta gagatagaga agttaggggt tattgggaga gggataaagt 960
tggttccaat gagttggttt ataggtcagg gacttgggaa gctgatcatg aaagagatgt 1020
taagaaagtg agtggtgga accgcgaatg cgatgtcaag gcagaggaga acaagagtaa 1080
15 gcctgaagaa cgtaaagaga aggttggtga agagcaagca aggcgatacc agttggatgt 1140
tcttgaacaa gctaaagcga aaaacacgat tgctttcctt gagaccggtg ctggaaagac 1200
acttatcgcg attcttctta ttaaaagtgt tcataaggat ctgatgagcc agaacagaaa 1260
aatgctctcg gtgttcttgg ttcccaaagt gcctttgggt tatcagcaag cagaagtgat 1320
ccgtaatcaa acttgttttc aagttggaca ttattgtggt gagatgggac aggacttttg 1380
20 ggattctcga aggtggcaac gagagtttga gtctaagcag gttctagtta tgacagcaca 1440
aattctgttg aatatactga gacacagtat cattagaatg gaaacaattg atcttcttat 1500
tctcgacgag tgtcaccacg ctgtcaagaa acatccatac tctttagtga tgtcagagtt 1560
ttaccataca actcctaaag ataaaagacc tgccatcttt ggaatgactg cttcgctgt 1620
taatttaaag ggtgtttcaa gccaaagtaga ttgtgcgata aagatacgta acctcgagac 1680
25 caagtggat tctacggttt gtactataaa agatcgaaaa gaattagaga aacatgtgcc 1740
tatgccttca gagatagtcg tcgagtatga caaagctgct actatgtgggt ctcttcatga 1800
gacaataaag caaatgattg cagctgttga agaagcggca caagcaagtt caaggaaaag 1860
caagtggcaa tttatggggg ctagggatgc tggagcaaag gatgaattga gacaggttta 1920
tggcgctctc gaaagaacgg agagcgatgg tgctgccaat ttgattcata aacttagagc 1980
30 tatcaattat actcttgctg aattgggtca atgggtgtgct tacaaggtgg gacaatcatt 2040
cttgtctgct ttgcaaagtg atgagagggt gaatttccaa gtcgacgtga agtttcaaga 2100

atcatacctc agtgaggtgg tgtcactctt gcaatgtgag cttctggaag gcgctgctgc 2160
tgaaaaagtc gcggcggaag ttggcaaacc agaaaatggt aatgcacatg acgagatgga 2220
ggaggggagag ctccctgatg atcctgtggt ctcgggaggg gagcacgttg atgaagtaat 2280
aggcgccgca gtggctgatg ggaaagttac tccaaaagta caatcattga tcaaactact 2340
5 cctcaaatat cagcacacag ctgattttcg agctattggt ttcgttgaga ggggtggtgc 2400
tgctttggtt cttcctaagg tttttcgga gctgccttcg cttagtttta tacggtgtgc 2460
cagcatgatt ggacacaata acagccagga gatgaaatca tctcaaagtc aggatacaat 2520
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acttgatatt aggcaatgta acgttggtat gcgtttcgac cttgcaaaga cgggtgctggc 2640
10 atacattcag tctcgtggcc gggcaagaaa gcctggatca gactacatac tcatggttga 2700
gagaggaaat gtatctcacg cagcgttcct aaggaatgct aggaacagtg aggagacact 2760
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cttgaattcc gcggttggtc ttgtacattt ctactgctct cagcttcctg gtgacaggta 2940
15 tgcaatcctt cgtcctgagt ttagcatgga gaagcatgaa aagcctgggg gccacacgga 3000
atattcatgt aggttcacg ttccttgcaa tgcaccgttt gaaatacttg agggctcctgt 3060
ttgcagttca atgcgtcttg cacaacaggc tgtatgttta gctgcttgca agaaactgca 3120
tgagatgggt gcatttaccg atatgctatt accggacaaa ggaagtggtc aagacgctga 3180
gaaggctgac caagatgatg aaggtagacc tgttcctgga actgctagac atagagagtt 3240
20 ctatcctgaa ggtgtggcgg atgtacttaa gggagaatgg gtttcatctg gaaaggaagt 3300
ttgtgagagc tcaaagctat tccatttata catgtataat gtcagatgtg tagattttgg 3360
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gctggatgca gaggtattat cgatgtctat ggatctttat gttgctcggg ccatgatcac 3480
taaagcatct cttgctttca agggatcact tgatattaca gaaaaccagc tatcatctct 3540
25 aaaaaagttt catgtgaggt taatgagtat cgtgttggat gttgatgttg aaccctccac 3600
gacaccatgg gatcctgcaa aggcctacct gtttgcctt gttactgaca atacgtctat 3660
ggaaccata aaagggatca actgggaatt ggttgaaaag attacgaaa ccacagcgtg 3720
ggacaaccct cttcagagag ctcgccccga tgtatatctc gggactaatg agagaactct 3780
tggtggggac agaagggaat atgggttttg taaacttcgt cacaacattg tatttgggca 3840
30 gaaatctcac ccaacttatg gtattagagg agctgttgca tccttcgatg ttgtgagagc 3900
ttctggattg ttacctgtga gagatgcttt tgagaaggaa gtagaagagg atttatcaaa 3960

aggaaaattg atgatggctg atgggtgcat gggtgcagaa gatccttattg ggaaaatagt 4020
gacagccgca cattccggga agcggtttta cgtagattca atttgttatg acatgagtgc 4080
agaaacatct ttccttagga aagagggata tcttgggtccc ctagagtaca acacgtacgc 4140
tgactattac aagcaaaagt atggagtga tttgaactgt aagcaacaac ctttgattaa 4200
5 aggacgtggt gtttcgtatt gcaagaacct tctttctcct cggtttgaac agtcagggtga 4260
atctgagaca gtccttgata agacatatta cgtgtttctt ccacctgaac tatgcgttgt 4320
gcatccgctt tggggttcac ttatccgagg tgctcagagg ttaccctcta taatgagaag 4380
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atcaaagatt cttgaagcct tgactgccgc ctctgcccag gaaacgttct gctacgagag 4500
10 agctgagctt ttaggagatg cgtatctaaa atgggttggt agtcgttttc tgtttctcaa 4560
gtatcctcaa aagcacgagg gtcagcttac aaggatgagg caacaaatgg ttagtaatat 4620
ggttctttat cagtttgctc tggttaaagg gcttcagtca tatatccagg cggatcgatt 4680
cgccccgtct aggtgggtctg ctctgggtgt gcctccggtt ttcgacgagg acacaaaaga 4740
tgaggatct tegtttttcg atgaagagca aaaacctgtt tccgaggaaa acagcgatgt 4800
15 gtttgaagat ggggagatgg aggatggtga actagagggt gatttgagtt cgtaccgagt 4860
tttatctagc aaaacgttag ctgatgttgt tgaggctttg attggtgttt attacgtcga 4920
agggggtaag attgcagcta atcatttgat gaaatggatt gggattcacg tggaggatga 4980
tcctgatgaa gtcgatggaa cattgaaaaa tgtaaatgtt ccagagagtg tgctcaagag 5040
catcgacttt gttggtcttg agagagctct taaatatgag tttaaagaga aaggtcttct 5100
20 tgttgaagct ataacacatg cttcaagacc atcttcaggt gtttcgtgtt accagagatt 5160
ggaatttggt ggtgacgagg tcttgatca tctcatcaca agacatctat ttttcacata 5220
cacaagcctt cctcctggtc ggtaacaga tcttcgagct gcagcgggta acaacgagaa 5280
ttttgctcgc gttgcgggta aacataaact ccacttgtag ctctgctacg gttcaagcgc 5340
cctcgaaaaa cagattcggg aatttgtgaa ggaggttcaa accgagtcac cgaaaccggg 5400
25 gtttaactct tttggtttgg gagactgcaa agcaccaaaa gttcttgagg acattgttga 5460
atctattgca ggtgctatct tcttgatag tggaaaagat acaactgctg cttggaaggt 5520
ttttcaacct ttgcttcagc ccatggtgac accagagaca cttccaatgc atccggtgcg 5580
agagctacaa gagcgggtgcc agcaacaagc agaagggtta gaatacaaag cgagtaggag 5640
tggtaacaca gcgactgtgg aagttttcat cgacgggtgt caagttggag tagcgcaaaa 5700
30 cccgcagaag aaaatggctc aaaagctagc tgcgaggaa gcacttgag ctttgaaaga 5760
gaaagaaata gcagaatcaa aggagaagca tatcaacaac ggtaatgcg gagaggatca 5820

agcgagaat gagaatggga acaagaagaa tgggcatcag ccgtttacga gacaaacgtt 5880
 gaatgatatt tgtttgagga agaattggcc aatgccttct tacagatgtg tgaaagaagg 5940
 aggaccggct catgcaaaga gatttacgtt tggggtaaga gttaatacga gcgatagagg 6000
 atggaccgat gagtgtattg gcgagccaat gccgagtgtt aagaaagcta aggattcagc 6060
 5 tgcggttctt ctacttgagc ttttaaataa aactttttct tgattctttt actctcttca 6120
 acgagatgta gtcattacat tttaaacctt aaaaccatag tgggtgtagt gttttaaaaa 6180
 aaaa 6184

The isolated cDNA has a 5727 bp open reading frame (ORF), a
 10 374 bp 5'-untranslated region (UTR), a 74 bp 3'-UTR and nine adenines at the 3'-
 end likely to be from the poly-A tail. The cDNA sequence confirmed the
 presence of 19 introns and 20 exons. A map of the chromosomal region
 overlapping *SIN1* is shown in Figure 1. RS10, nga59, 12D7L and ACC2 are DNA
 sequence markers. Numbers within brackets are numbers of cross-overs between
 15 La-*er* and Columbia chromosomes. yUP20D1 and yUP12D7 are YAC clones;
 T4J2, T25K16 and F7I23 are BAC clones. The lower portion of the diagram
 shows intron-exon boundaries of *SIN1* gene. The arrow above the *sus1-1* shows
 that site of insertion of the linked T-DNA in *sus1-1*. That the open reading frame
 corresponds to *SIN1* gene is substantiated by the findings that the *sus1*, *sin1-1*, and
 20 *sin1-2* mutant phenotypes are traceable to DNA mutations in the *SIN1* gene. The
sus1 mutation is due to DNA insertion within the 5th exon of the *SIN1* gene. The
sin1-1 and *sin1-2* phenotypes are the result of single-base pair changes, in exon 3
 and exon 4, respectively. A single C to T transition in *sin1-1* and a T to A
 transversion in *sin1-2* reading frames were detected.

25 Also suitable as an isolated nucleic acid molecule according to the
 present invention is a nucleic acid which has a nucleotide sequence that is at least
 55% similar to the nucleotide sequence of SEQ. ID. No. 1 by basic BLAST using
 default parameters analysis. Also suitable as an isolated nucleic acid molecule
 according to the present invention is an isolated nucleic acid molecule encoding a
 30 short integuments1 protein, wherein the nucleic acid hybridizes to the nucleotide
 sequence of SEQ. ID. No. 1 under stringent conditions characterized by a
 hybridization buffer comprising 0.9M sodium citrate buffer at a temperature of
 45°C.

	Met	Val	Met	Glu	Asp	Glu	Pro	Arg	Glu	Ala	Thr	Ile	Lys	Pro	Ser	Tyr
5	1				5					10						15
	Trp	Leu	Asp	Ala	Cys	Glu	Asp	Ile	Ser	Cys	Asp	Leu	Ile	Asp	Asp	Leu
				20					25					30		
10	Val	Ser	Glu	Phe	Asp	Pro	Ser	Ser	Val	Ala	Val	Asn	Glu	Ser	Thr	Asp
			35					40					45			
	Glu	Asn	Gly	Val	Ile	Asn	Asp	Phe	Phe	Gly	Gly	Ile	Asp	His	Ile	Leu
		50					55					60				
15	Asp	Ser	Ile	Lys	Asn	Gly	Gly	Gly	Leu	Pro	Asn	Asn	Gly	Val	Ser	Asp
	65					70					75					80
	Thr	Asn	Ser	Gln	Ile	Asn	Glu	Val	Thr	Val	Thr	Pro	Gln	Val	Ile	Ala
20					85					90						95
	Lys	Glu	Thr	Val	Lys	Glu	Asn	Gly	Leu	Gln	Lys	Asn	Gly	Gly	Lys	Arg
				100					105					110		
25	Asp	Glu	Phe	Ser	Lys	Glu	Glu	Gly	Asp	Lys	Asp	Arg	Lys	Arg	Ala	Arg
			115					120					125			
	Val	Cys	Ser	Tyr	Gln	Ser	Glu	Arg	Ser	Asn	Leu	Ser	Gly	Arg	Gly	His
		130					135					140				
30	Val	Asn	Asn	Ser	Arg	Glu	Gly	Asp	Arg	Phe	Met	Asn	Arg	Lys	Arg	Thr
	145					150				155						160
	Arg	Asn	Trp	Asp	Glu	Ala	Gly	Asn	Asn	Lys	Lys	Lys	Arg	Glu	Cys	Asn
35					165					170						175
	Asn	Tyr	Arg	Arg	Asp	Gly	Arg	Asp	Arg	Glu	Val	Arg	Gly	Tyr	Trp	Glu
				180					185					190		

	Arg Asp Lys Val Gly Ser Asn Glu Leu Val Tyr Arg Ser Gly Thr Trp	
	195	200 205
5	Glu Ala Asp His Glu Arg Asp Val Lys Lys Val Ser Gly Gly Asn Arg	
	210	215 220
	Glu Cys Asp Val Lys Ala Glu Glu Asn Lys Ser Lys Pro Glu Glu Arg	
	225	230 235 240
10	Lys Glu Lys Val Val Glu Glu Gln Ala Arg Arg Tyr Gln Leu Asp Val	
	245	250 255
	Leu Glu Gln Ala Lys Ala Lys Asn Thr Ile Ala Phe Leu Glu Thr Gly	
15	260	265 270
	Ala Gly Lys Thr Leu Ile Ala Ile Leu Leu Ile Lys Ser Val His Lys	
	275	280 285
20	Asp Leu Met Ser Gln Asn Arg Lys Met Leu Ser Val Phe Leu Val Pro	
	290	295 300
	Lys Val Pro Leu Val Tyr Gln Gln Ala Glu Val Ile Arg Asn Gln Thr	
	305	310 315 320
25	Cys Phe Gln Val Gly His Tyr Cys Gly Glu Met Gly Gln Asp Phe Trp	
	325	330 335
	Asp Ser Arg Arg Trp Gln Arg Glu Phe Glu Ser Lys Gln Val Leu Val	
30	340	345 350
	Met Thr Ala Gln Ile Leu Leu Asn Ile Leu Arg His Ser Ile Ile Arg	
	355	360 365
	Met Glu Thr Ile Asp Leu Leu Ile Leu Asp Glu Cys His His Ala Val	
35	370	375 380
	Lys Lys His Pro Tyr Ser Leu Val Met Ser Glu Phe Tyr His Thr Thr	
	385	390 395 400
40	Pro Lys Asp Lys Arg Pro Ala Ile Phe Gly Met Thr Ala Ser Pro Val	

	405	410	415
	Asn Leu Lys Gly Val Ser Ser Gln Val Asp Cys Ala Ile Lys Ile Arg		
	420	425	430
5	Asn Leu Glu Thr Lys Leu Asp Ser Thr Val Cys Thr Ile Lys Asp Arg		
	435	440	445
	Lys Glu Leu Glu Lys His Val Pro Met Pro Ser Glu Ile Val Val Glu		
10	450	455	460
	Tyr Asp Lys Ala Ala Thr Met Trp Ser Leu His Glu Thr Ile Lys Gln		
	465	470	475 480
15	Met Ile Ala Ala Val Glu Glu Ala Ala Gln Ala Ser Ser Arg Lys Ser		
	485	490	495
	Lys Trp Gln Phe Met Gly Ala Arg Asp Ala Gly Ala Lys Asp Glu Leu		
	500	505	510
20	Arg Gln Val Tyr Gly Val Ser Glu Arg Thr Glu Ser Asp Gly Ala Ala		
	515	520	525
	Asn Leu Ile His Lys Leu Arg Ala Ile Asn Tyr Thr Leu Ala Glu Leu		
25	530	535	540
	Gly Gln Trp Cys Ala Tyr Lys Val Gly Gln Ser Phe Leu Ser Ala Leu		
	545	550	555 560
30	Gln Ser Asp Glu Arg Val Asn Phe Gln Val Asp Val Lys Phe Gln Glu		
	565	570	575
	Ser Tyr Leu Ser Glu Val Val Ser Leu Leu Gln Cys Glu Leu Leu Glu		
	580	585	590
35	Gly Ala Ala Ala Glu Lys Val Ala Ala Glu Val Gly Lys Pro Glu Asn		
	595	600	605
	Gly Asn Ala His Asp Glu Met Glu Glu Gly Glu Leu Pro Asp Asp Pro		
40	610	615	620

Val Val Ser Gly Gly Glu His Val Asp Glu Val Ile Gly Ala Ala Val
625 630 635 640

5 Ala Asp Gly Lys Val Thr Pro Lys Val Gln Ser Leu Ile Lys Leu Leu
645 650 655

Leu Lys Tyr Gln His Thr Ala Asp Phe Arg Ala Ile Val Phe Val Glu
660 665 670

10 Arg Val Val Ala Ala Leu Val Leu Pro Lys Val Phe Ala Glu Leu Pro
675 680 685

Ser Leu Ser Phe Ile Arg Cys Ala Ser Met Ile Gly His Asn Asn Ser
15 690 695 700

Gln Glu Met Lys Ser Ser Gln Met Gln Asp Thr Ile Ser Lys Phe Arg
705 710 715 720

20 Asp Gly His Val Thr Leu Leu Val Ala Thr Ser Val Ala Glu Glu Gly
725 730 735

Leu Asp Ile Arg Gln Cys Asn Val Val Met Arg Phe Asp Leu Ala Lys
740 745 750

25 Thr Val Leu Ala Tyr Ile Gln Ser Arg Gly Arg Ala Arg Lys Pro Gly
755 760 765

Ser Asp Tyr Ile Leu Met Val Glu Arg Gly Asn Val Ser His Ala Ala
30 770 775 780

Phe Leu Arg Asn Ala Arg Asn Ser Glu Glu Thr Leu Arg Lys Glu Ala
785 790 795 800

35 Ile Glu Arg Thr Asp Leu Ser His Leu Lys Asp Thr Ser Arg Leu Ile
805 810 815

Ser Ile Asp Ala Val Pro Gly Thr Val Tyr Lys Val Glu Ala Thr Gly
820 825 830

40

	Ala Met Val Ser Leu Asn Ser Ala Val Gly Leu Val His Phe Tyr Cys		
	835	840	845
5	Ser Gln Leu Pro Gly Asp Arg Tyr Ala Ile Leu Arg Pro Glu Phe Ser		
	850	855	860
	Met Glu Lys His Glu Lys Pro Gly Gly His Thr Glu Tyr Ser Cys Arg		
	865	870	875 880
10	Leu Gln Leu Pro Cys Asn Ala Pro Phe Glu Ile Leu Glu Gly Pro Val		
	885	890	895
	Cys Ser Ser Met Arg Leu Ala Gln Gln Ala Val Cys Leu Ala Ala Cys		
	900	905	910
15	Lys Lys Leu His Glu Met Gly Ala Phe Thr Asp Met Leu Leu Pro Asp		
	915	920	925
	Lys Gly Ser Gly Gln Asp Ala Glu Lys Ala Asp Gln Asp Asp Glu Gly		
20	930	935	940
	Glu Pro Val Pro Gly Thr Ala Arg His Arg Glu Phe Tyr Pro Glu Gly		
	945	950	955 960
25	Val Ala Asp Val Leu Lys Gly Glu Trp Val Ser Ser Gly Lys Glu Val		
	965	970	975
	Cys Glu Ser Ser Lys Leu Phe His Leu Tyr Met Tyr Asn Val Arg Cys		
	980	985	990
30	Val Asp Phe Gly Ser Ser Lys Asp Pro Phe Leu Ser Glu Val Ser Glu		
	995	1000	1005
	Phe Ala Ile Leu Phe Gly Asn Glu Leu Asp Ala Glu Val Leu Ser Met		
35	1010	1015	1020
	Ser Met Asp Leu Tyr Val Ala Arg Ala Met Ile Thr Lys Ala Ser Leu		
	1025	1030	1035 1040
40	Ala Phe Lys Gly Ser Leu Asp Ile Thr Glu Asn Gln Leu Ser Ser Leu		

	1045	1050	1055
	Lys Lys Phe His Val Arg Leu Met Ser Ile Val Leu Asp Val Asp Val		
	1060	1065	1070
5	Glu Pro Ser Thr Thr Pro Trp Asp Pro Ala Lys Ala Tyr Leu Phe Val		
	1075	1080	1085
	Pro Val Thr Asp Asn Thr Ser Met Glu Pro Ile Lys Gly Ile Asn Trp		
10	1090	1095	1100
	Glu Leu Val Glu Lys Ile Thr Lys Thr Thr Ala Trp Asp Asn Pro Leu		
	1105	1110	1115 1120
15	Gln Arg Ala Arg Pro Asp Val Tyr Leu Gly Thr Asn Glu Arg Thr Leu		
	1125	1130	1135
	Gly Gly Asp Arg Arg Glu Tyr Gly Phe Gly Lys Leu Arg His Asn Ile		
	1140	1145	1150
20	Val Phe Gly Gln Lys Ser His Pro Thr Tyr Gly Ile Arg Gly Ala Val		
	1155	1160	1165
	Ala Ser Phe Asp Val Val Arg Ala Ser Gly Leu Leu Pro Val Arg Asp		
25	1170	1175	1180
	Ala Phe Glu Lys Glu Val Glu Glu Asp Leu Ser Lys Gly Lys Leu Met		
	1185	1190	1195 1200
30	Met Ala Asp Gly Cys Met Val Ala Glu Asp Leu Ile Gly Lys Ile Val		
	1205	1210	1215
	Thr Ala Ala His Ser Gly Lys Arg Phe Tyr Val Asp Ser Ile Cys Tyr		
	1220	1225	1230
35	Asp Met Ser Ala Glu Thr Ser Phe Pro Arg Lys Glu Gly Tyr Leu Gly		
	1235	1240	1245
	Pro Leu Glu Tyr Asn Thr Tyr Ala Asp Tyr Tyr Lys Gln Lys Tyr Gly		
40	1250	1255	1260

Val Asp Leu Asn Cys Lys Gln Gln Pro Leu Ile Lys Gly Arg Gly Val
1265 1270 1275 1280

5 Ser Tyr Cys Lys Asn Leu Leu Ser Pro Arg Phe Glu Gln Ser Gly Glu
1285 1290 1295

Ser Glu Thr Val Leu Asp Lys Thr Tyr Tyr Val Phe Leu Pro Pro Glu
1300 1305 1310

10 Leu Cys Val Val His Pro Leu Ser Gly Ser Leu Ile Arg Gly Ala Gln
1315 1320 1325

Arg Leu Pro Ser Ile Met Arg Arg Val Glu Ser Met Leu Leu Ala Val
15 1330 1335 1340

Gln Leu Lys Asn Leu Ile Ser Tyr Pro Ile Pro Thr Ser Lys Ile Leu
1345 1350 1355 1360

20 Glu Ala Leu Thr Ala Ala Ser Cys Gln Glu Thr Phe Cys Tyr Glu Arg
1365 1370 1375

Ala Glu Leu Leu Gly Asp Ala Tyr Leu Lys Trp Val Val Ser Arg Phe
1380 1385 1390

25 Leu Phe Leu Lys Tyr Pro Gln Lys His Glu Gly Gln Leu Thr Arg Met
1395 1400 1405

Arg Gln Gln Met Val Ser Asn Met Val Leu Tyr Gln Phe Ala Leu Val
30 1410 1415 1420

Lys Gly Leu Gln Ser Tyr Ile Gln Ala Asp Arg Phe Ala Pro Ser Arg
1425 1430 1435 1440

35 Trp Ser Ala Pro Gly Val Pro Pro Val Phe Asp Glu Asp Thr Lys Asp
1445 1450 1455

Gly Gly Ser Ser Phe Phe Asp Glu Glu Gln Lys Pro Val Ser Glu Glu
1460 1465 1470

40

Asn Ser Asp Val Phe Glu Asp Gly Glu Met Glu Asp Gly Glu Leu Glu
1475 1480 1485

5 Gly Asp Leu Ser Ser Tyr Arg Val Leu Ser Ser Lys Thr Leu Ala Asp
1490 1495 1500

Val Val Glu Ala Leu Ile Gly Val Tyr Tyr Val Glu Gly Gly Lys Ile
1505 1510 1515 1520

10 Ala Ala Asn His Leu Met Lys Trp Ile Gly Ile His Val Glu Asp Asp
1525 1530 1535

Pro Asp Glu Val Asp Gly Thr Leu Lys Asn Val Asn Val Pro Glu Ser
1540 1545 1550

15 Val Leu Lys Ser Ile Asp Phe Val Gly Leu Glu Arg Ala Leu Lys Tyr
1555 1560 1565

Glu Phe Lys Glu Lys Gly Leu Leu Val Glu Ala Ile Thr His Ala Ser
20 1570 1575 1580

Arg Pro Ser Ser Gly Val Ser Cys Tyr Gln Arg Leu Glu Phe Val Gly
1585 1590 1595 1600

25 Asp Ala Val Leu Asp His Leu Ile Thr Arg His Leu Phe Phe Thr Tyr
1605 1610 1615

Thr Ser Leu Pro Pro Gly Arg Leu Thr Asp Leu Arg Ala Ala Ala Val
1620 1625 1630

30 Asn Asn Glu Asn Phe Ala Arg Val Ala Val Lys His Lys Leu His Leu
1635 1640 1645

Tyr Leu Arg His Gly Ser Ser Ala Leu Glu Lys Gln Ile Arg Glu Phe
35 1650 1655 1660

Val Lys Glu Val Gln Thr Glu Ser Ser Lys Pro Gly Phe Asn Ser Phe
1665 1670 1675 1680

40 Gly Leu Gly Asp Cys Lys Ala Pro Lys Val Leu Gly Asp Ile Val Glu

	1685	1690	1695
	Ser Ile Ala Gly Ala Ile Phe Leu Asp Ser Gly Lys Asp Thr Thr Ala		
	1700	1705	1710
5	Ala Trp Lys Val Phe Gln Pro Leu Leu Gln Pro Met Val Thr Pro Glu		
	1715	1720	1725
	Thr Leu Pro Met His Pro Val Arg Glu Leu Gln Glu Arg Cys Gln Gln		
10	1730	1735	1740
	Gln Ala Glu Gly Leu Glu Tyr Lys Ala Ser Arg Ser Gly Asn Thr Ala		
	1745	1750	1755 1760
15	Thr Val Glu Val Phe Ile Asp Gly Val Gln Val Gly Val Ala Gln Asn		
	1765	1770	1775
	Pro Gln Lys Lys Met Ala Gln Lys Leu Ala Ala Arg Asn Ala Leu Ala		
	1780	1785	1790
20	Ala Leu Lys Glu Lys Glu Ile Ala Glu Ser Lys Glu Lys His Ile Asn		
	1795	1800	1805
	Asn Gly Asn Ala Gly Glu Asp Gln Gly Glu Asn Glu Asn Gly Asn Lys		
25	1810	1815	1820
	Lys Asn Gly His Gln Pro Phe Thr Arg Gln Thr Leu Asn Asp Ile Cys		
	1825	1830	1835 1840
30	Leu Arg Lys Asn Trp Pro Met Pro Ser Tyr Arg Cys Val Lys Glu Gly		
	1845	1850	1855
	Gly Pro Ala His Ala Lys Arg Phe Thr Phe Gly Val Arg Val Asn Thr		
	1860	1865	1870
35	Ser Asp Arg Gly Trp Thr Asp Glu Cys Ile Gly Glu Pro Met Pro Ser		
	1875	1880	1885
	Val Lys Lys Ala Lys Asp Ser Ala Ala Val Leu Leu Leu Glu Leu Leu		
40	1890	1895	1900

Asn Lys Thr Phe Ser

1905

Analysis of this protein revealed a domain structure highly
5 suggestive of an RNA helicase (Company et al., "Requirement of the RNA
Helicase-Like Protein PRP22 for Release of Messenger RNA from
Spliceosomes," Nature 349:487-493 (1991); Linder et al., "Birth of the D-E-A-D
Box," Nature 337:121-122 (1989); Luking et al., "The Protein Family of RNA
Helicases," Crit. Rev. Biochem. Mol. Biol. 33:259-296 (1998); Martins et al.,
10 "Mutational Analysis of Vaccinia Virus Nucleoside Triphosphate
Phosphohydrolase I, a DNA-Dependent ATPase of the DExH Box Family,"
Journal of Virology 73:1302-1308 (1999), which are hereby incorporated by
reference), of which *Drosophila* maternal effect gene *Vasa* is a representative
(Rongo et al., "Germplasm Assembly and Germ Cell Migration in *Drosophila*,"
15 Cold Spring Harb. Symp. Quant. Biol. 62:1-11 (1997), which is hereby
incorporated by reference). Shown in the lower portion of Figure 1 is the
arrangement of functional motifs of the predicted SIN1 protein: a bipartite N-
terminal nuclear localization signal (NLS), an RNA helicase C domain, two
RNase III catalytic domains, a PIMS (for PIWI Middle domain-SHORT
20 INTEGUMENTS1, *PIWI* being a family of important plant developmental
proteins) motif, and two C-terminal repeats of a dsRNA binding domain. A
BLAST search yielded numerous high homology strikes of these domains, as
shown in Figure 2. Each of the three functional domains is strongly conserved
within its own family. For example, the helicase C motif shows strong similarity,
25 among others, to yeast *RRP3*, *DRS1* and fly *Vasa* products, RNase3 domains to
pombe *PAC1* or worm K12H4.8 (YM68), and dsRBD domains to *Drosophila*
Staufen products.

Fragments of the above protein are also encompassed by the
present invention. Suitable fragments can be produced by several means. In the
30 first, subclones of the gene encoding the protein of the present invention are
produced by conventional molecular genetic manipulation by subcloning gene
fragments. The subclones then are expressed *in vitro* or *in vivo* in bacterial cells
to yield a smaller protein or peptide.

In another approach, based on knowledge of the primary structure of the protein of the present invention, fragments of the gene of the present invention may be synthesized by using the PCR technique together with specific sets of primers chosen to represent particular portions of the protein. These then
5 would be cloned into an appropriate vector for increased expression of an accessory peptide or protein.

Chemical synthesis can also be used to make suitable fragments. Such a synthesis is carried out using known amino acid sequences for the protein of the present invention. These fragments can then be separated by conventional
10 procedures (e.g., chromatography, SDS-PAGE) and used in the methods of the present invention.

Variants may also (or alternatively) be prepared by, for example, the deletion or addition of amino acids that have minimal influence on the properties, secondary structure, and hydrophobic nature of the polypeptide. For
15 example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification, or identification of the polypeptide.

20 The present invention also relates to an expression vector containing a DNA molecule encoding a short integuments1 protein. The nucleic acid molecule of the present invention may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art. In preparing a DNA vector for expression, the various DNA sequences
25 may normally be inserted or substituted into a bacterial plasmid. Any convenient plasmid may be employed, which will be characterized by having a bacterial replication system, a marker which allows for selection in a bacterium and generally one or more unique, conveniently located restriction sites. Numerous plasmids, referred to as transformation vectors, are available for plant
30 transformation. The selection of a vector will depend on the preferred transformation technique and target species for transformation. A variety of vectors are available for stable transformation using *Agrobacterium tumefaciens*, a soilborne bacterium that causes crown gall. Crown gall are characterized by

tumors or galls that develop on the lower stem and main roots of the infected plant. These tumors are due to the transfer and incorporation of part of the bacterium plasmid DNA into the plant chromosomal DNA. This transfer DNA (T-DNA) is expressed along with the normal genes of the plant cell. The plasmid
5 DNA, pTI, or Ti-DNA, for "tumor inducing plasmid," contains the *vir* genes necessary for movement of the T-DNA into the plant. The T-DNA carries genes that encode proteins involved in the biosynthesis of plant regulatory factors, and bacterial nutrients (opines). The T-DNA is delimited by two 25 bp imperfect direct repeat sequences called the "border sequences." By removing the oncogene
10 and opine genes, and replacing them with a gene of interest, it is possible to transfer foreign DNA into the plant without the formation of tumors or the multiplication of *Agrobacterium tumefaciens*. Fraley, et al., "Expression of Bacterial Genes in Plant Cells," Proc. Nat'l Acad. Sci., 80:4803-4807 (1983), which is hereby incorporated by reference.

15 Further improvement of this technique led to the development of the binary vector system. Bevan, M., "Binary *Agrobacterium* Vectors for Plant Transformation," Nucleic Acids Res. 12:8711-8721 (1984), which is hereby incorporated by reference. In this system, all the T-DNA sequences (including the borders) are removed from the pTi, and a second vector containing T-DNA is
20 introduced into *Agrobacterium tumefaciens*. This second vector has the advantage of being replicable in *E. coli* as well as *A. tumefaciens*, and contains a multiclonal site that facilitates the cloning of a transgene. An example of a commonly used vector is pBin19. Frisch, et al., "Complete Sequence of the Binary Vector Bin19," Plant Molec. Biol. 27:405-409 (1995), which is hereby incorporated by reference. Any
25 appropriate vectors now known or later described for genetic transformation are suitable for use with the present invention.

U.S. Patent No. 4,237,224 issued to Cohen and Boyer, which is hereby incorporated by reference, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and
30 ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including procaryotic organisms and eucaryotic cells grown in tissue culture.

In one aspect of the present invention, the nucleic acid molecule of the present invention is incorporated into an appropriate vector in the sense direction, such that the open reading frame is properly oriented for the expression of the encoded protein under control of a promoter of choice.

5 Certain "control elements" or "regulatory sequences" are also incorporated into the vector-construct. Those non-translated regions of the vector, promoters, 5' and 3' untranslated regions-which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any
10 number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used.

A constitutive promoter is a promoter that directs expression of a gene throughout the development and life of an organism. Examples of some constitutive promoters that are widely used for inducing expression of transgenes
15 include the nopoline synthase (NOS) gene promoter, from *Agrobacterium tumefaciens*, (U.S. Patent 5034322 to Rogers et al., which is hereby incorporated by reference), the cauliflower mosaic virus (CaMv) 35S and 19S promoters (U.S. Patent No. 5,352,605 to Fraley et al., which is hereby incorporated by reference), those derived from any of the several actin genes, which are known to be
20 expressed in most cells types (U.S. Patent No. 6,002,068 to Privalle et al., which is hereby incorporated by reference), and the ubiquitin promoter, which is a gene product known to accumulate in many cell types.

An inducible promoter is a promoter that is capable of directly or indirectly activating transcription of one or more DNA sequences or genes in
25 response to an inducer. In the absence of an inducer, the DNA sequences or genes will not be transcribed. The inducer can be a chemical agent, such as a metabolite, growth regulator, herbicide or phenolic compound, or a physiological stress directly imposed upon the plant such as cold, heat, salt, toxins, or through the action of a pathogen or disease agent such as a virus or fungus. A plant cell
30 containing an inducible promoter may be exposed to an inducer by externally applying the inducer to the cell or plant such as by spraying, watering, heating, or by exposure to the operative pathogen. An example of an appropriate inducible promoter for use in the present invention is a glucocorticoid-inducible promoter

(Schena et al., "A Steroid-Inducible Gene Expression System for Plant Cells," Proc. Natl. Acad. Sci. 88:10421-5 (1991), which is hereby incorporated by reference). Expression of the SIN1 protein is induced in the plants transformed with the *SIN1* gene when the transgenic plants are brought into contact with

5 nanomolar concentrations of a glucocorticoid, or by contact with dexamethasone, a glucocorticoid analog. Schena et al., "A Steroid-Inducible Gene Expression System for Plant Cells," Proc. Natl. Acad. Sci. USA 88:10421-5 (1991); Aoyama et al., "A Glucocorticoid-Mediated Transcriptional Induction System in Transgenic Plants," Plant J. 11: 605-612 (1997), and McNellis et al.,

10 "Glucocorticoid-Inducible Expression of a Bacterial Avirulence Gene in Transgenic Arabidopsis Induces Hypersensitive Cell Death," Plant J. 14(2):247-57 (1998), which are hereby incorporated by reference. In addition, inducible promoters include promoters that function in a tissue specific manner to regulate the gene of interest within selected tissues of the plant. Examples of such tissue

15 specific promoters include seed, flower, or root specific promoters as are well known in the field (U.S. Patent No. 5,750,385 to Shewmaker et al., which is hereby incorporated by reference).

The DNA construct of the present invention also includes an operable 3' regulatory region, selected from among those which are capable of

20 providing correct transcription termination and polyadenylation of mRNA for expression in the host cell of choice, operably linked to a DNA molecule which encodes for a protein of choice. A number of 3' regulatory regions are known to be operable in plants. Exemplary 3' regulatory regions include, without limitation, the nopaline synthase 3' regulatory region (Fraley, et al., "Expression

25 of Bacterial Genes in Plant Cells," Proc. Nat'l Acad. Sci. USA 80:4803-4807 (1983), which is hereby incorporated by reference) and the cauliflower mosaic virus 3' regulatory region (Odell, et al., "Identification of DNA Sequences Required for Activity of the Cauliflower Mosaic Virus 35S Promoter," Nature 313(6005):810-812 (1985), which is hereby incorporated by reference). Virtually

30 any 3' regulatory region known to be operable in plants would suffice for proper expression of the coding sequence of the DNA construct of the present invention.

The vector of choice, promoter, and an appropriate 3' regulatory region can be ligated together to produce the plasmid of the present invention

using well known molecular cloning techniques as described in Sambrook et al.,
5 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor
Press, NY (1989), and Ausubel, F. M. et al. (1989) Current Protocols in Molecular
Biology, John Wiley & Sons, New York, N.Y., which are hereby incorporated by
reference.

Once the DNA construct of the present invention has been
prepared, it is ready to be incorporated into a host cell. Recombinant molecules
can be introduced into cells via transformation, particularly transduction,
conjugation, mobilization, or electroporation. The DNA sequences are cloned
10 into the host cell using standard cloning procedures known in the art, as described
by Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition,
Cold Springs Laboratory, Cold Springs Harbor, New York (1989), which is
hereby incorporated by reference. Suitable host cells include, but are not limited
to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like. Preferably
15 the host cells are either a bacterial cell or a plant cell.

Accordingly, another aspect of the present invention relates to a
method of making a recombinant cell. Basically, this method is carried out by
transforming a plant cell with a DNA construct of the present invention under
conditions effective to yield transcription of the DNA molecule in the plant cell.
20 Preferably, the DNA construct of the present invention is stably inserted into the
genome of the recombinant plant cell as a result of the transformation.

One approach to transforming plant cells with a DNA construct of
the present invention is particle bombardment (also known as biolistic
transformation) of the host cell. This can be accomplished in one of several ways.
25 The first involves propelling inert or biologically active particles at cells. This
technique is disclosed in U.S. Patent Nos. 4,945,050, 5,036,006, and 5,100,792,
all to Sanford, et al., which are hereby incorporated by reference. Generally, this
procedure involves propelling inert or biologically active particles at the cells
under conditions effective to penetrate the outer surface of the cell and to be
30 incorporated within the interior thereof. When inert particles are utilized, the
vector can be introduced into the cell by coating the particles with the vector
containing the heterologous DNA. Alternatively, the target cell can be surrounded
by the vector so that the vector is carried into the cell by the wake of the particle.

Biologically active particles (e.g., dried bacterial cells containing the vector and heterologous DNA) can also be propelled into plant cells. Other variations of particle bombardment, now known or hereafter developed, can also be used.

Transient expression in protoplasts allows quantitative studies of gene expression since the population of cells is very high (on the order of 10^6). To deliver DNA inside protoplasts, several methodologies have been proposed, but the most common are electroporation (Fromm et al., "Expression of Genes Transferred Into Monocot and Dicot Plants by Electroporation," Proc. Natl. Acad. Sci. USA 82:5824-5828 (1985), which is hereby incorporated by reference) and polyethylene glycol (PEG) mediated DNA uptake (Krens et al., "In Vitro Transformation of Plant Protoplasts with Ti-Plasmid DNA," Nature 296:72-74 (1982), which is hereby incorporated by reference). During electroporation, the DNA is introduced into the cell by means of a reversible change in the permeability of the cell membrane due to exposure to an electric field. PEG transformation introduces the DNA by changing the elasticity of the membranes. Unlike electroporation, PEG transformation does not require any special equipment and transformation efficiencies can be equally high. Another appropriate method of introducing the gene construct of the present invention into a host cell is fusion of protoplasts with other entities, either minicells, cells, lysosomes, or other fusible lipid-surfaced bodies that contain the chimeric gene. Fraley, et al., Proc. Natl. Acad. Sci. USA, 79:1859-63 (1982), which is hereby incorporated by reference.

Stable transformants are preferable for the methods of the present invention. An appropriate method of stably introducing the DNA construct into plant cells is to infect a plant cell with *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* previously transformed with the DNA construct. Under appropriate conditions known in the art, the transformed plant cells are grown to form shoots or roots, and develop further into plants. In one embodiment of the present invention stable transformants are generated using *Agrobacterium* using the "dipping" method, a modification of the vacuum infiltration method as described in Bent et al., "Floral Dip: A Simplified Method for *Agrobacterium*-Mediated Transformation of *Arabidopsis thaliana*," Plant J. 16:735-43 (1998), which is hereby incorporated by reference.

Plant tissues suitable for transformation include, but are not limited to, floral buds, leaf tissue, root tissue, meristems, zygotic and somatic embryos, megasporos, and anthers.

After transformation, the transformed plant cells can be selected
5 and regenerated. Preferably, transformed cells are first identified using a selection
marker simultaneously introduced into the host cells along with the DNA
construct of the present invention. The most widely used reporter gene for gene
fusion experiments has been *uidA*, a gene from *Escherichia coli* that encodes the
 β -glucuronidase protein, also known as GUS. Jefferson et al., "GUS Fusions: β
10 Glucuronidase as a Sensitive and Versatile Gene Fusion Marker in Higher Plants,"
EMBO Journal 6:3901-3907 (1987), which is hereby incorporated by reference.
GUS is a 68.2 kd protein that acts as a tetramer in its native form. It does not
require cofactors or special ionic conditions, although it can be inhibited by
divalent cations like Cu^{2+} or Zn^{2+} . GUS is active in the presence of thiol reducing
15 agents like β -mercaptoethanol or dithiothreitol (DTT).

In order to evaluate GUS activity, several substrates are available.
The most commonly used are 5 bromo-4 chloro-3 indolyl glucuronide (X-Gluc)
and 4 methyl-umbelliferyl-glucuronide (MUG). The reaction with X-Gluc
generates a blue color that is useful in histochemical detection of the gene activity.
20 For quantification purposes, MUG is preferred, because the umbelliferyl radical
emits fluorescence under UV stimulation, thus providing better sensitivity and
easy measurement by fluorometry (Jefferson et al., "GUS Fusions: β
Glucuronidase as a Sensitive and Versatile Gene Fusion Marker in Higher Plants,"
EMBO Journal 6:3901-3907 (1987), which is hereby incorporated by reference).
25 Other suitable selection markers include, without limitation, markers encoding for
antibiotic resistance, such as the *nptII* gene which confers kanamycin resistance
(Fraley, et al., Proc. Natl. Acad. Sci. USA, 80:4803-4807 (1983), which is hereby
incorporated by reference) and the *dhfr* gene, which confers resistance to
methotrexate (Bourouis et al., EMBO J. 2:1099-1104 (1983), which is hereby
30 incorporated by reference). A number of antibiotic-resistance markers are known
in the art and others are continually being identified. Any known antibiotic-
resistance marker can be used to transform and select transformed host cells in

accordance with the present invention. Cells or tissues are grown on a selection medium containing an antibiotic, whereby generally only those transformants expressing the antibiotic resistance marker continue to grow. Similarly, enzymes providing for production of a compound identifiable by luminescence, such as luciferase, are useful. The selection marker employed will depend on the target species; for certain target species, different antibiotics, herbicide, or biosynthesis selection markers are preferred.

Once a recombinant plant cell or tissue has been obtained, it is possible to regenerate a full-grown plant therefrom. Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing transformed explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

Plant regeneration from cultured protoplasts is described in Evans, et al., Handbook of Plant Cell Cultures, Vol. 1: (MacMillan Publishing Co., New York, 1983); and Vasil I.R. (ed.), Cell Culture and Somatic Cell Genetics of Plants, Acad. Press, Orlando, Vol. I, 1984, and Vol. III (1986), which are hereby incorporated by reference.

It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to, all major species of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, sugarcane, and non-fruit bearing trees such as poplar, rubber, Paulownia, pine, and elm.

After the DNA construct is stably incorporated in transgenic plants, it can be transferred to other plants by sexual crossing or by preparing cultivars. With respect to sexual crossing, any of a number of standard breeding techniques can be used depending upon the species to be crossed. Cultivars can be propagated in accord with common agricultural procedures known to those in the field. Alternatively, transgenic seeds are recovered from the transgenic plants. The seeds can then be planted in the soil and cultivated using conventional procedures to produce transgenic plants.

Since loss of function (*Sin1* mutation) delays flowering, a gain of function, for example, by overexpression of *Sin1* gene, should promote early flowering. Accordingly, another aspect of the present invention relates to a method of increasing fertility in plants by transforming plants with the nucleic acid of the present invention. Fertility can be functionally (albeit simplistically) defined as the onset of reproductive maturity. By reducing the time from vegetative to floral stage in plants, overall breeding time can be reduced. Thus, the nucleic acid molecule of the present invention, as a regulator of flowering time, can be used to accelerate flowering in plants. This involves transforming plants with the nucleic acid of the present invention in an expression vector as described above, operably linked to an inducible promoter, such as the glucocorticoid inducible promoter. Transgenic plants in which an inducible promoter is present are treated with the suitable inducing agent (e.g., dexamethasone for the glucocorticoid inducible promoter) to induce flowering. Inducing SIN1 protein expression earlier in the development of the plant than normal accelerates early flowering, such that breeding time can be reduced. In addition, induction of flowering eliminates dependence upon external factors for flowering such as temperature and light (Coupland G., "Genetic and Environmental Control of Flowering Time in *Arabidopsis*," Mol. Gen. Genet. 242:81-89 (1995), which is hereby incorporated by reference), which are beyond the control of the average farmer. Early flowering plant lines may be especially useful for cultivation in short daylight environments.

In another aspect of the present invention, the fecundity of plants can be increased by overexpression of the nucleic acid of the present invention, under control of a constitutive promoter. Fecundity relates to reproductive

maturity in combination with the total number of seeds a mature plant can produce. Thus, decreasing the time to flowering with expression of the protein of the present invention is one factor of increased fecundity, as it increases time spent in the adult phase. The other factor, seed development, is also related to expression of the protein of the present invention, as this protein, when maternally expressed, appears to coordinate the expression of zygotic pattern formation in the embryo. In this aspect of the present invention, the nucleic acid of the present invention is inserted into an expression vector, as described above, operably linked to a constitutive promoter, for example, the CaMV35S promoter. Increased expression of the protein of the present invention, which functions both in the formation of seeds and in the mother plant in embryo formation, can result in increased fecundity.

The present invention also relates to a method of decreasing fertility in plants. Because it may be commercially desirable to produce sterile female progeny, or plants with low expression of the protein of the present invention, transgenic plants can be produced in which the expression of this protein is down-regulated, or even entirely "switched off." In one aspect of the present invention, the nucleic acid of the present invention is replaced in the above-described expression vector by an antisense nucleic acid molecule which is complementary to the nucleic acid of the present invention or a fragment thereof. Antisense technology is commonplace to those skilled in the art, and the preparation of a vector and transgenic plants containing an antisense nucleic acid would be followed as described above. Transgenic plants are produced as described above, which exhibit a phenotype deficient in the nucleic acid of the present invention.

In another aspect of the present invention, the silencing of the constitutive *SINI* gene involves the use of double-stranded RNA ("dsRNA") interference ("RNAi"), a procedure which has recently been shown to induce potent and specific post-translational gene silencing in many organisms. See Boshier et al., "RNA Interference: Genetic Wand and Genetic Watchdog," Nat Cell Biol 2:E31-6 (2000); Tavernarakis et al., "Heritable and Inducible Genetic Interference by Double-Stranded RNA encoded by Transgenes," Nat Genetics 24:180-3 (2000), which are hereby incorporated by reference. To construct

transformation vectors that produce RNAs capable of duplex formation, two nucleic acid sequences according to the present invention, one in the sense and the other in the antisense orientation, are operably linked, and placed under the control of a strong viral promoter, such as CaMV 35S. The construct is introduced into the genome of *Arabidopsis thaliana* by *Agrobacterium*-mediated transformation (Chuang et al., "Specific and Heritable Genetic Interference by Double-Stranded RNA in *Arabidopsis thaliana*," Proc. Natl. Acad. Sci. USA 97:4985-90 (2000), which is hereby incorporated by reference), causing specific and heritable genetic interference, as evidenced by *SIN1* deficient phenotype.

In another aspect of the present invention, plant lines containing insertional mutations are produced, disrupting the endogenous *SIN1* gene and thereby creating a *SIN1* protein deficient plant with decreased fertility. This is accomplished by making use of well-characterized plant transposons such as the maize *Activator* ("Ac") and *Dissociation* ("Ds") family of transposable elements. The family is comprised of the autonomous element Ac, and the nonautonomous Ds element. Ds elements are not capable of autonomous transposition, but can be *trans*-activated to transpose by Ac. Hehl et al., "Induced Transposition of *Ds* by a Stable *Ac* in Crosses of Transgenic Tobacco Plants," Mol. Gen. Genet. 217:53-59 (1989), which is hereby incorporated by reference. Thus, transposable elements, such as Ac/Ds of maize, can be operably linked to the nucleic acid of the present invention, transferred to other plants to generate a relatively small number of anchor plants (such as 500), and then to produce a much larger number of secondary insertional-mutant plant lines. The Ac/Ds system has been improved by the use of enhancer- and gene-trap plasmids (Sundaresan et al., "Patterns of Gene Action in Plant Development Revealed by Enhancer Trap and Gene Trap Transposable Elements," Genes & Develop. 9:1797-1810 (1995), which is hereby incorporated by reference), which allow disrupted genes with no phenotype to be detected by expression of a reporter gene (such as *Gus*). After insertion of the mutant genes, plants are screened using marker genes and appropriate crosses made to produce stable mutant plant lines. Sundaresan et al., "Patterns of Gene Action in Plant Development Revealed by Enhancer Trap and Gene Trap Transposable Elements," Genes & Develop. 9:1797-1810 (1995), which is hereby incorporated by reference.

In another aspect of the present invention, the point mutations identified herein which result in *SIN1* deficient phenotypes *sus1*, *sin1-1*, and *sin1-2* can be prepared and used in the construct of the present invention to create transgenic plants and seeds carrying these point mutation alleles. The *sus1* mutation is predicted to delete most of the functional domains of the SIN1 protein. The *sin1-1* mutation produces a 415-proline to serine change in the protein; the *sin1-2* produces a 431-isoleucine to lysine change within the C-terminus helicase domain. Molecular modeling indicates that these two mutations perturb the RNA binding face of the DEHX box of the helicase C domain. Homozygous *sin1-1* or *sin1-2* mutation in *Arabidopsis* causes female sterility due to two separate phenotypic defects, and *sin1* mutants are late flowering. The allelic DNA can be synthetically produced, according to methods known to those in the art, or by inserting the above disclosed point mutations in the nucleic acid of the present invention, thereby creating plants with decreased fertility and decreased/late flowering.

In various aspects of the present invention the *SIN1* gene is either up- or down-regulated, or turned off entirely. In order to ascertain the increase or decrease in SIN1 protein expression resulting from genetic manipulation, measurement of the production of the SIN1 protein in plant tissues is carried out following transformation. Western blot, or any similar method of protein detection is appropriate, using either polyclonal or monoclonal antibodies to the protein of the present invention. Polyclonal antibodies can be produced by procedures well-known to those skilled in the art, such as those disclosed in E. Harlow, et al, editors Antibodies: A Laboratory Manual (1988), which is hereby incorporated by reference. The preparation of monoclonal antibodies, as well as Fab and $F(ab')_2$ fragments, also useful in protein detection methods, can be produced by various commonly used methods, such as those described in Goding, Monoclonal Antibodies: Principles and Practice, pp. 98-118, New York: Academic Press (1983), which is hereby incorporated by reference.

Although preferred embodiments have been depicted and described in detail herein, it will be apparent to those skilled in the relevant art that various modifications, additions, substitutions, and the like can be made without departing

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